REMARKS

The specification has been amended to correct typographical errors.

Claim 1 has been amended to restrict it to an isolated nucleic acid encoding the polypeptide having the amino acid sequence of SEQ ID NO:5.

Claim 3 has been amended to restrict it to the nucleotide sequences set forth in SEQ ID NO:1, 3 or 4.

Claims 2, 4-10, 19-21, 14-25, 27, 28 and 31-36 have been canceled without prejudice to filing in one or more continuation applications for the canceled subject matter of the elected invention or divisional applications for the canceled subject matter of the restricted inventions.

Claim 29 has been amended to depend from claim 26.

It is submitted that these amendments do not constitute new matter and their entry is requested.

Pending Claims

In view of the above amendments, claims 1, 3, 11-13, 26, 29 and 30 remain pending. Claims to the restricted inventions have been canceled.

Objections to Specification and Claims

The Examiner objected to the specification paragraph [0092] and claims 1 and 3 for typographical errors. The specification has been amended to correct the typographical errors and the objected language has been deleted from claims 1 and 3. Applicants submit that these amendments obviate these objections. Withdrawal of these objections is requested.

Rejection Under 35 U.S.C. § 112, second paragraph

The Examiner rejected claims 3, 26 and 36 under 35 U.S.C. § 112, second paragraph for being indefinite because of a phrase in the last part of claim 3. Claim 3 has been amended to delete

the objected phrase. Applicants submit that claim 3 as amended is definite. Withdrawal of this rejection is requested.

Rejection Under 35 U.S.C. § 112, first paragraph

The Examiner rejected claims 1, 3, 5, 11-13, 25-30 and 35-36 under 35 U.S.C. § 112, first paragraph for lack of written description. The specification clearly describes nucleic acids encoding the polypeptide having the amino acid sequence of SEQ ID NO:5 as now required by claim 1, and clearly describes the nucleic acids having the nucleotide sequences of SEQ ID NO:1, 3 and 4 as now required by claim 3. Claims 11-13, 26, 29 and 30 depend from claims 1 and 3. Claims 5 (in view of the amendment to claim 1), 25 (in view of the amendment to claim 3), 27, 28, 35 and 36 have been canceled. Thus, Applicants submit that the specification provides a written description of the claimed subject matter. Withdrawal of this rejection is requested.

Rejection Under 35 U.S.C. § 112, first paragraph

The Examiner rejected claims 3, 5, 11-13, 25-30 and 35-36 under 35 U.S.C. § 112, first paragraph for lack of enablement. In making this rejection, the Examiner contends that the specification does not provide enough evidence to demonstrate that the polypeptide of SEQ ID NO:5 is responsible for resistance to *Xanthomonas* and is thus the Xa31 gene. This contention is based on three points: (1) the specification shows that the coding regions are the same between the resistant and susceptible alleles, (2) the specification says that the expression patterns are similar and (3) the specification teaches that the functional terminator are identical between the two alleles. In the response to the previous Office Action Applicants argued that the specification as a whole clearly demonstrates that the coding region imparts resistance to *Xanthomonas* in transgenic plants based on the mapping, cloning and sequencing of the resistance allele and the identification of the coding sequence in Examples 1-7. In reply, the Examiner contends that the specification fails to provide guidance on why the resistant allele can provide resistance while the susceptible allele cannot. The Examiner further contends that the specification does not provide evidence that the

protein of SEQ ID NO:5 is responsible for the resistance. Applicants submit that the Examiner is in error in this rejection and submit that the amended claims are fully enabled by the specification.

First, it is well known to the skilled artisan that it is not the nucleic acid that directly imparts a phenotypic trait but that it is the protein encoded by the nucleic acid that imparts this phenotypic trait, in this case resistance to *Xanthomonas*. The nucleic acid may include control elements that control the expression of the encoded protein, i.e., the transcription of the gene and the translation into the protein. However, if the protein is not expressed, there is no expression of the phenotypic trait, *Xanthomonas* resistance in the present invention. Therefore, the skilled artisan knows that it is the protein of SEQ ID NO:5 that imparts the *Xanthomonas* resistance, especially in view of all of the evidence present in the present application. Applicants submit that any nucleic acid that encodes the protein of SEQ ID NO:5 would impart *Xanthomonas* resistance.

The evidence in the specification clearly demonstrates that it is the protein of SEQ ID NO:5 that imparts the resistance to *Xanthomonas*. Specifically, the specification shows the mapping, cloning and sequencing of the resistance allele and the identification of the coding sequence in Examples 1-7. Example 6 describes complementation studies and genomic cloning of the resistant allele. Transgenic plants transformed with a contig containing the resistant allele were resistant to *Xanthomonas* and this resistance was inherited. See, paragraph [0079] and Table 3. These studies demonstrated that the cloned resistant allele imparted resistance to *Xanthomonas* in transgenic plants. Example 7 describes the isolation of cDNA clones from a cDNA library that was used for screening for the expressed genes in the resistant and susceptible alleles. The cDNA that was isolated encodes the protein of SEQ ID NO:5. As stated in Example 7, no other expressed region within the resistant allele was found. The specification clearly teaches that Applicants isolated the *Xa31* gene by positional cloning strategy and transformation approaches. Genetic complementation mapped the *Xa31* gene to the 5198-bp genomic clone from IRBB31. Only one gene or transcriptional unit was identified in the 5198-bp region. As the transcriptional unit was activated upon inoculation with incompatible pathogens, the encoded protein from the mRNA transcript is the Xa31 protein. The Examiner has not provided any sound scientific evidence or reasoning to dispute

the teachings of the specification. *In re Wright*, 27 U.S.P.Q.2d 1510, 1513 (Fed. Cir.1993); *In re Marzocchi*, 169 USPQ 367, 370 (CCPA 1973) ("It is incumbent upon the Patent Office, whenever a rejection on this basis [i.e. doubt of the objective truth of statements in the specification] is made, to explain why it doubts the truth or accuracy of any statement in a supporting disclosure and to back up assertions of its own with acceptable evidence or reasoning which is inconsistent with the contested statement."). Thus, Applicants submit that the specification as a whole clearly teaches to a skilled artisan that the polypeptide of SEQ ID NO:5 is the polypeptide that imparts resistance to *Xanthomonas*.

Contrary to the Examiner's contention, the specification clearly provides guidance to the skilled artisan as to why the resistant allele can provide resistance to *Xanthomonas* while the susceptible allele cannot. The specification clearly teaches that the promoter regions of the resistant allele and the susceptible allele are different. See, page 33, paragraph [0087] and Figure 9. The promoter region of the susceptible allele has two copies of a 25 bp element that is located 20 bp upstream of the TATA box, whereas the promoter region of the resistant allele has a single copy of this element. In addition, the promoter region of the susceptible allele has three nucleotides deleted 3' of the end of the TATA box compared to the promoter region of the resistant allele. These differences in the promoter region of the resistant and susceptible alleles provide guidance to a skilled artisan as to why there is a difference between these alleles. The Examiner has not provided any sound scientific evidence or reasoning to dispute this teaching of the specification. *In re Wright*, 27 U.S.P.Q.2d 1510, 1513 (Fed. Cir.1993); *In re Marzocchi*, 169 USPQ 367, 370 (CCPA 1973). In addition and as noted in the prior response, Gu et al. ("*R* gene expression induced by a type-III effector triggers disease resistance in rice," *Nature* **435**:1122-1125, 2005) confirms this guidance provided by the specification.

In addition, the specification provides guidance for preparing transgenic plants that impart resistance to *Xanthomonas*. Specifically, in paragraph [0047] *et seq.*, Applicants disclose that the polypeptide may be expressed from vectors containing a nucleic acid encoding the polypeptide operatively linked to a promoter. The promoter may be the native promoter from the resistant allele

or a promoter functional in the host cell, e.g., a promoter functional in a plant cell or plant. The promoter from the susceptible allele is not included in this description of promoters that can be used. Thus, the specification provides guidance on the use of the polypeptide of SEQ ID NO:5 and on imparting *Xanthomonas* resistance to a transgenic plant cell or plant. The Examiner has not provided any sound scientific evidence or reasoning to dispute the teachings of the specification. *In re Wright*, 27 U.S.P.Q.2d 1510, 1513 (Fed. Cir.1993); *In re Marzocchi*, 169 USPQ 367, 370 (CCPA 1973). Similarly, Gu et al. confirms this guidance provided by the specification.

Furthermore, in paragraph [0088], Applicants affirmatively state that the polypeptide of SEQ ID NO:5 is the polypeptide of the resistant allele. The Examiner has not provided any sound scientific evidence or reasoning to dispute this teaching of the specification. *In re Wright*, 27 U.S.P.Q.2d 1510, 1513 (Fed. Cir.1993); *In re Marzocchi*, 169 USPQ 367, 370 (CCPA 1973).

Thus, Applicants submit that the specification as a whole unequivocally teaches that the polypeptide of SEQ ID NO:5 is the polypeptide that imparts resistance to *Xanthomonas*. The specification provides evidence that the polypeptide of SEQ ID NO:5 is responsible for the *Xanthomonas* resistance in the mapping, cloning and sequencing of the resistance allele studies and in the complementation studies set fort in the Examples. Applicants further submit that the specification as a whole provides guidance to the skilled artisan as to why the resistant allele provides resistance to *Xanthomonas* while the susceptible allele cannot. The specification as a whole provides guidance that this difference is due to the differences in the promoters of the resistant and susceptible alleles.

In view of the above amendment and remarks, Applicants submit that the specification fully enables the claimed subject matter. Withdrawal of this rejection is requested.

Conclusion

In view of the above amendments and remarks, Applicants believe that the present claims satisfy the provisions of the patent statutes and are patentable over the cited prior art. Reconsideration of this application and early notice of allowance is requested. The Examiner is

invited to telephone the undersigned if it will assist in expediting the prosecution and allowance of the instant application.

Respectfully submitted,

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